Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:34:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524922.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524922.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:34:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	953,165
Mapped reads	826,163 / 86.68%
Unmapped reads	127,002 / 13.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,437 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	17,508 / 1.84%
Duplication rate	1.53%
Clipped reads	829,089 / 86.98%

2.2. ACGT Content

Number/percentage of A's	12,350,010 / 26.07%
Number/percentage of C's	8,534,890 / 18.01%
Number/percentage of T's	14,686,286 / 31%
Number/percentage of G's	11,806,884 / 24.92%
Number/percentage of N's	1,377 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1633

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

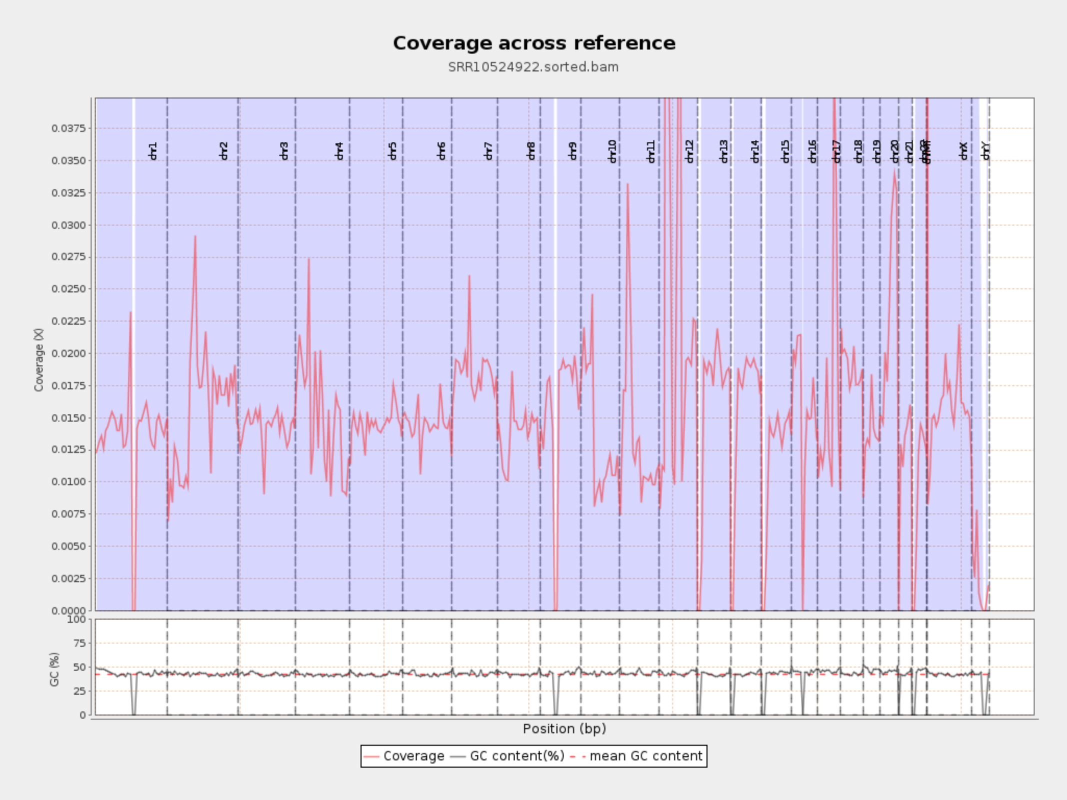
General error rate	0.48%
Mismatches	222,510
Insertions	2,653
Mapped reads with at least one insertion	0.32%
Deletions	7,222
Mapped reads with at least one deletion	0.87%
Homopolymer indels	43.11%

2.6. Chromosome stats

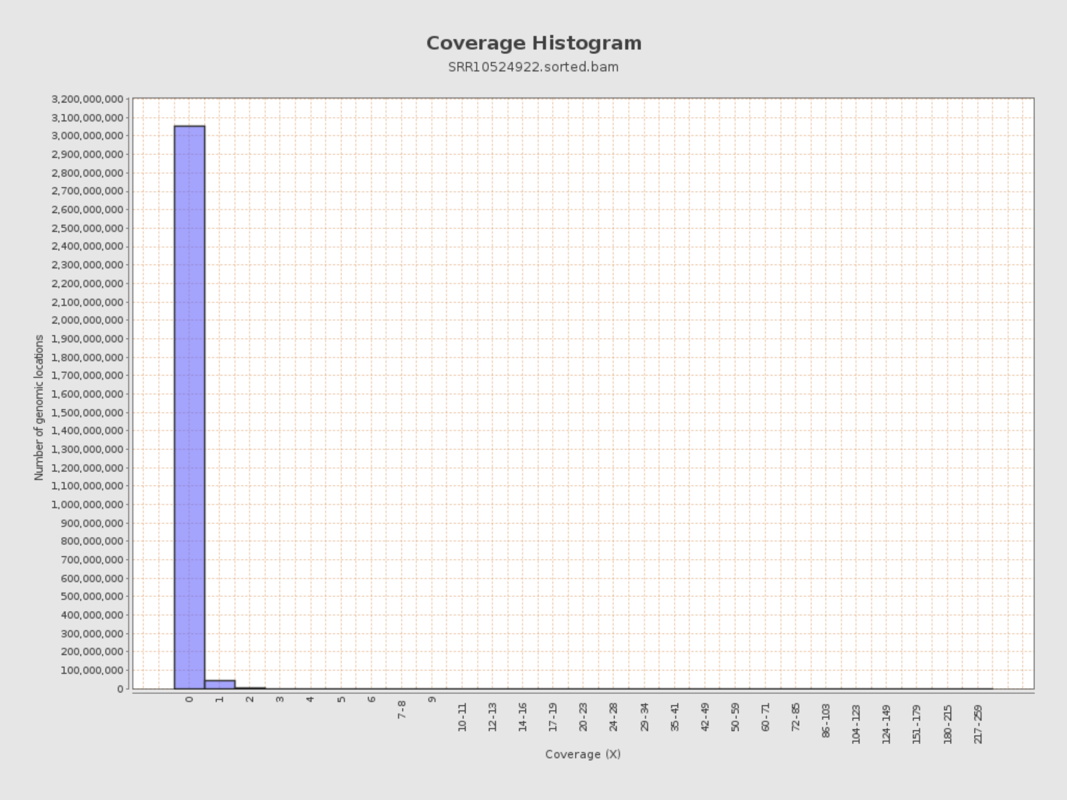
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3374494	0.0135	0.2478
chr2	243199373	3831507	0.0158	0.1725
chr3	198022430	2821490	0.0142	0.1246
chr4	191154276	2897790	0.0152	0.1377
chr5	180915260	2647839	0.0146	0.1273
chr6	171115067	2478767	0.0145	0.1321
chr7	159138663	2965534	0.0186	0.2068

chr8	146364022	2022603	0.0138	0.156
chr9	141213431	2180154	0.0154	0.1629
chr10	135534747	1843264	0.0136	0.1571
chr11	135006516	1818041	0.0135	0.1442
chr12	133851895	3542889	0.0265	0.18
chr13	115169878	1838864	0.016	0.1319
chr14	107349540	1670778	0.0156	0.1346
chr15	102531392	1184049	0.0115	0.1129
chr16	90354753	1394988	0.0154	0.1334
chr17	81195210	1426723	0.0176	0.1413
chr18	78077248	1476420	0.0189	0.2712
chr19	59128983	817446	0.0138	0.1919
chr20	63025520	1499097	0.0238	0.1644
chr21	48129895	597853	0.0124	0.1249
chr22	51304566	475044	0.0093	0.1004
chrMT	16571	7022	0.4238	0.7065
chrX	155270560	2446009	0.0158	0.142
chrY	59373566	132926	0.0022	0.0666

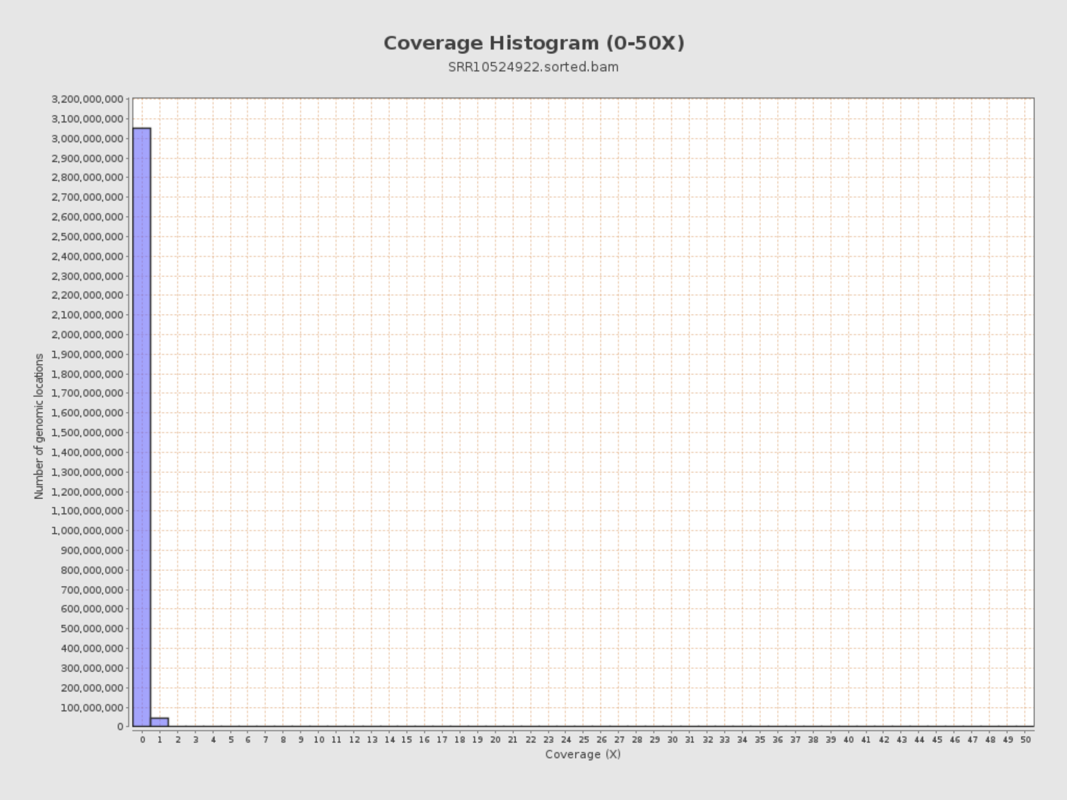
3. Results : Coverage across reference



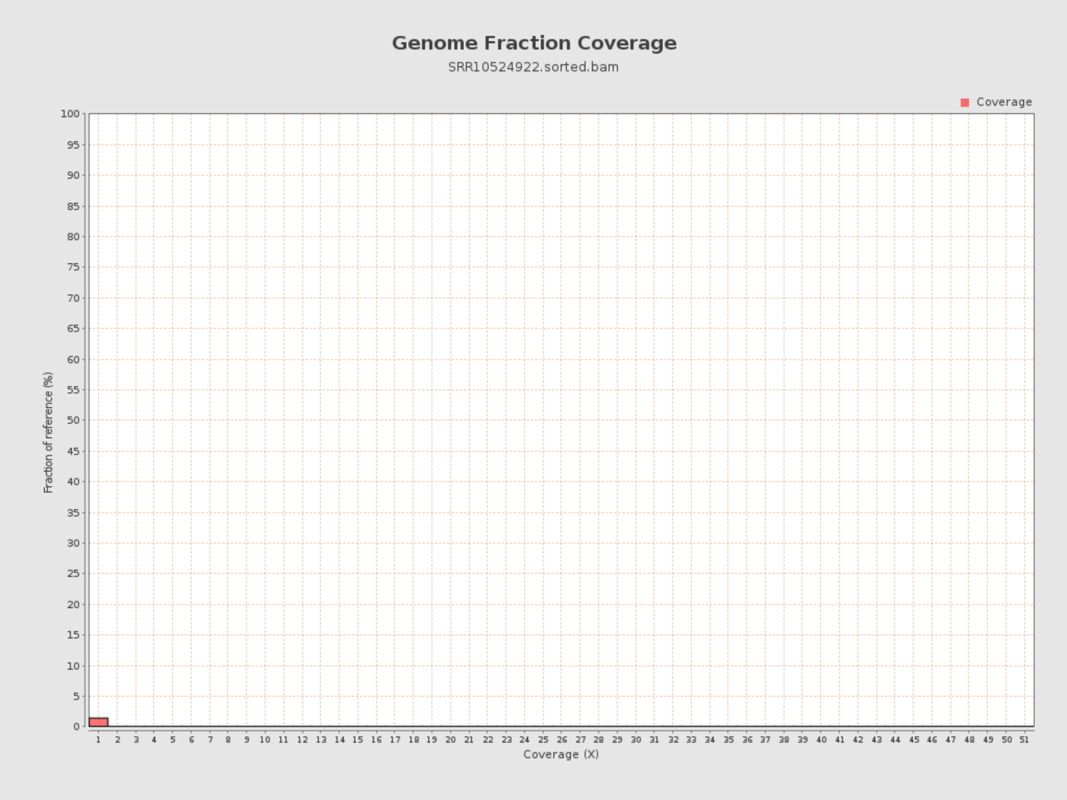
4. Results : Coverage Histogram



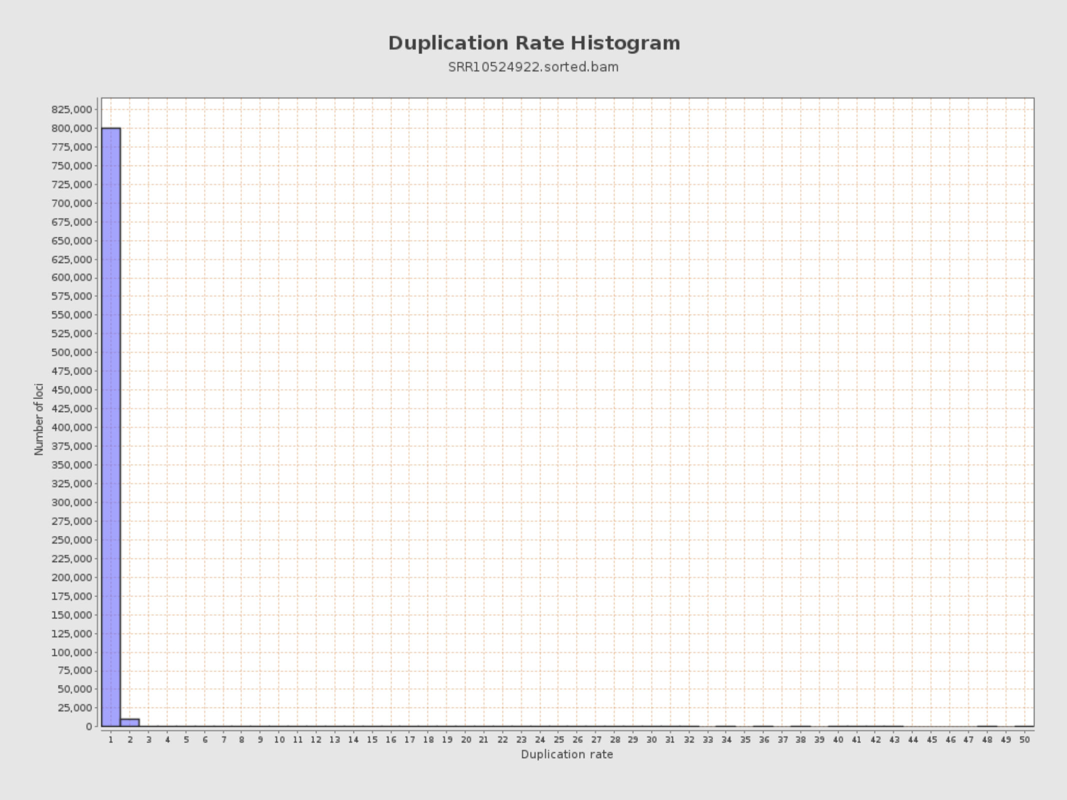
5. Results : Coverage Histogram (0-50X)



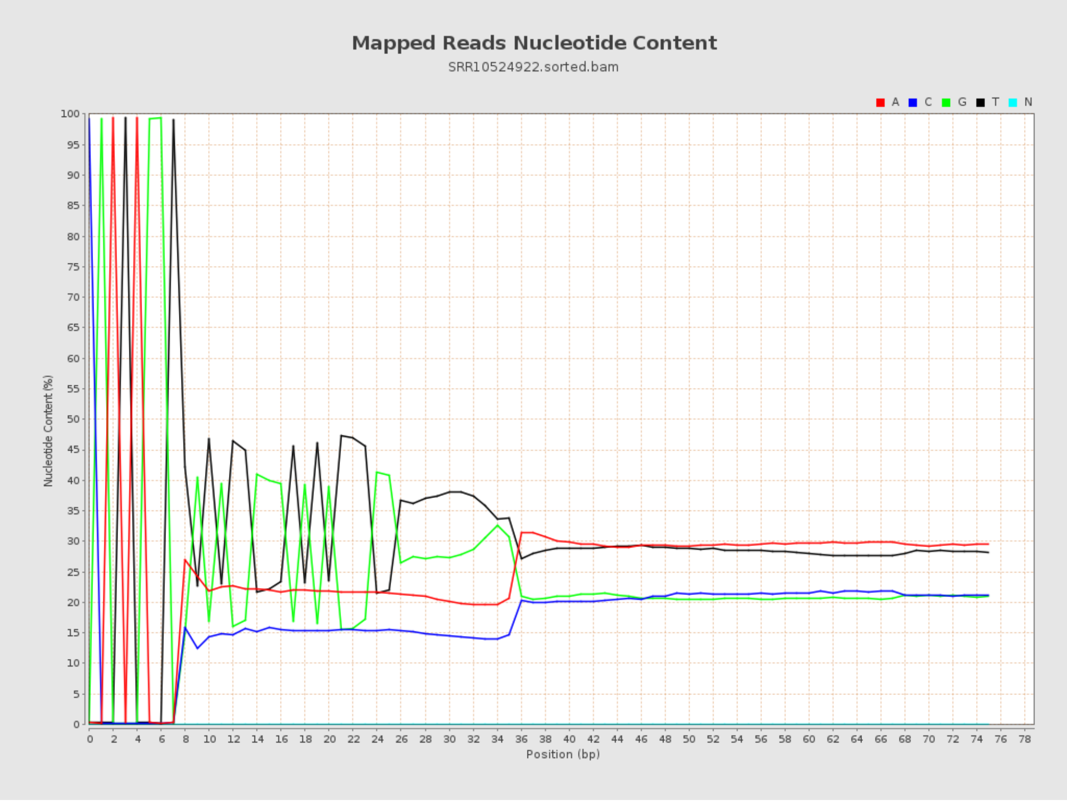
6. Results : Genome Fraction Coverage



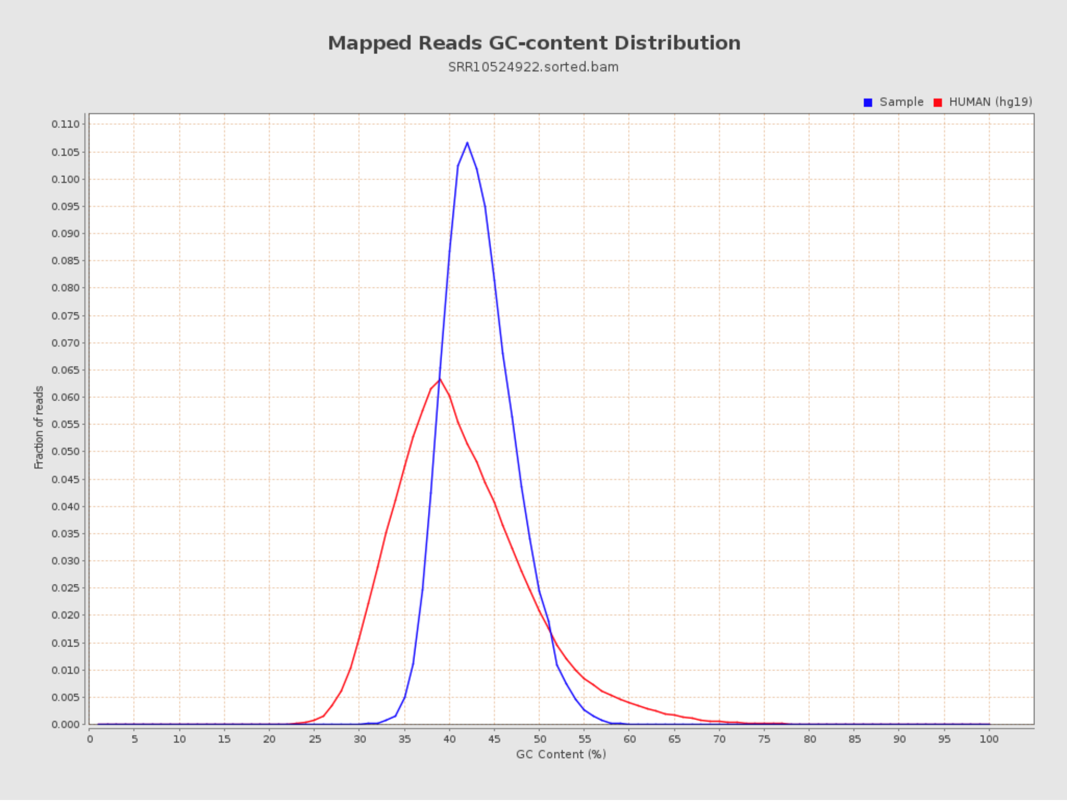
7. Results : Duplication Rate Histogram



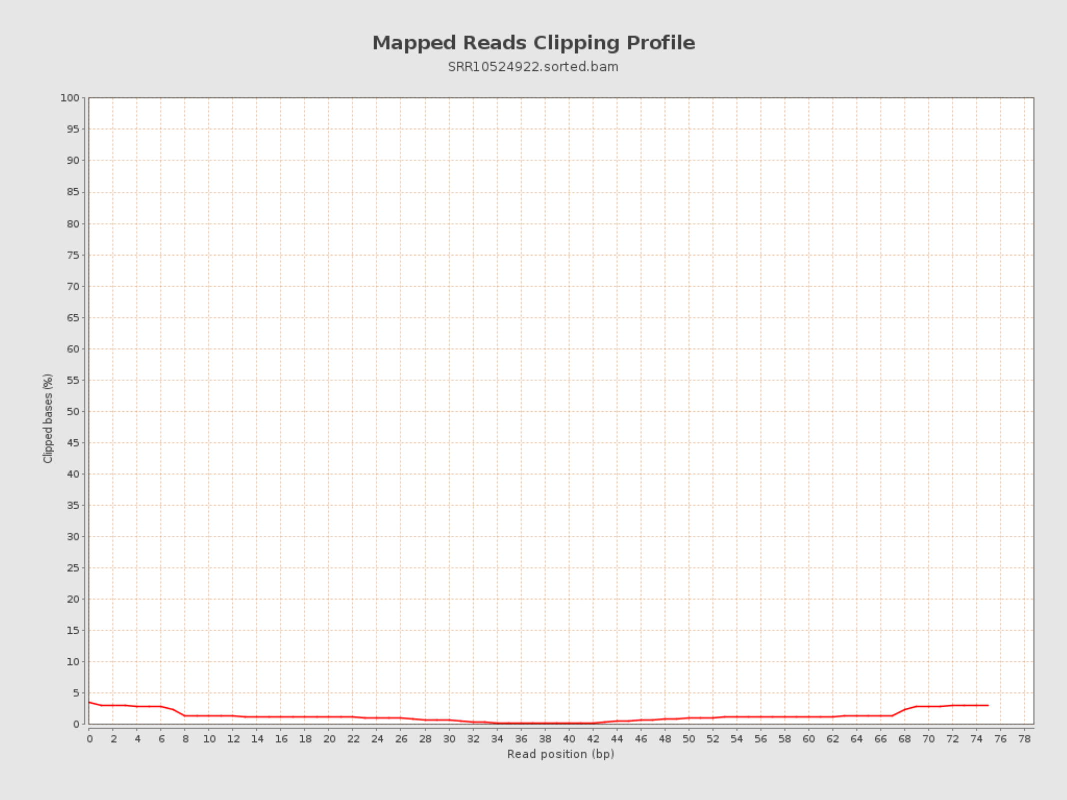
8. Results : Mapped Reads Nucleotide Content



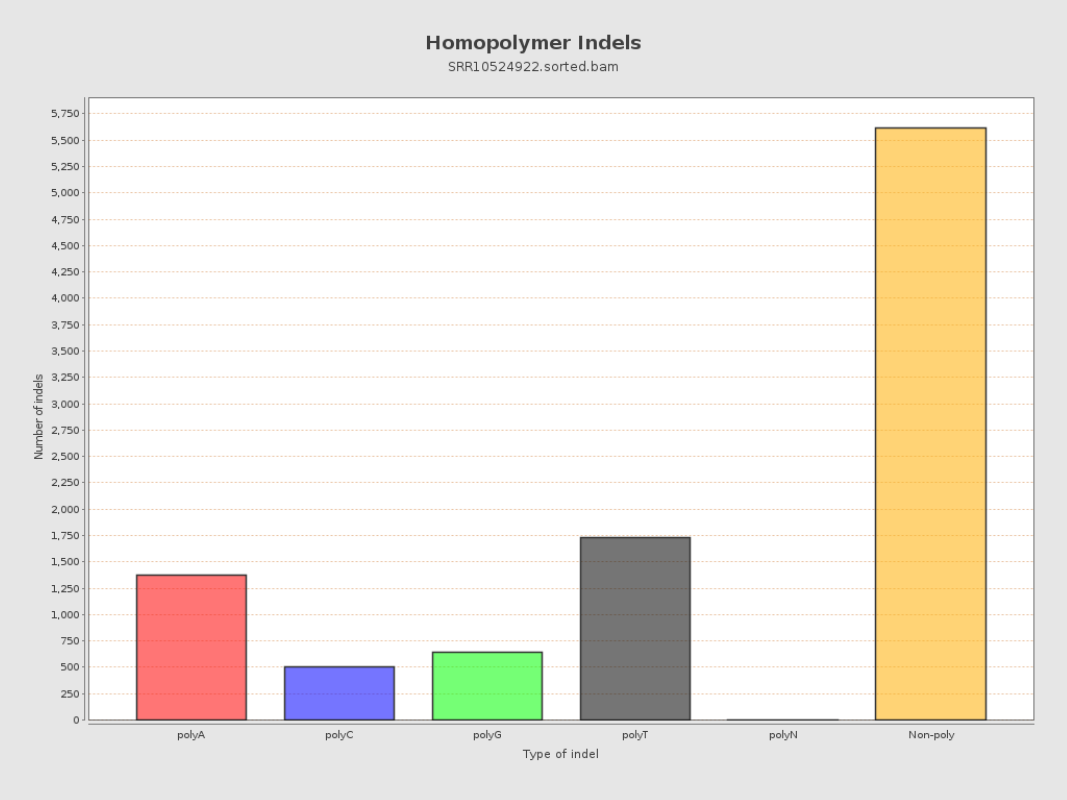
9. Results : Mapped Reads GC-content Distribution



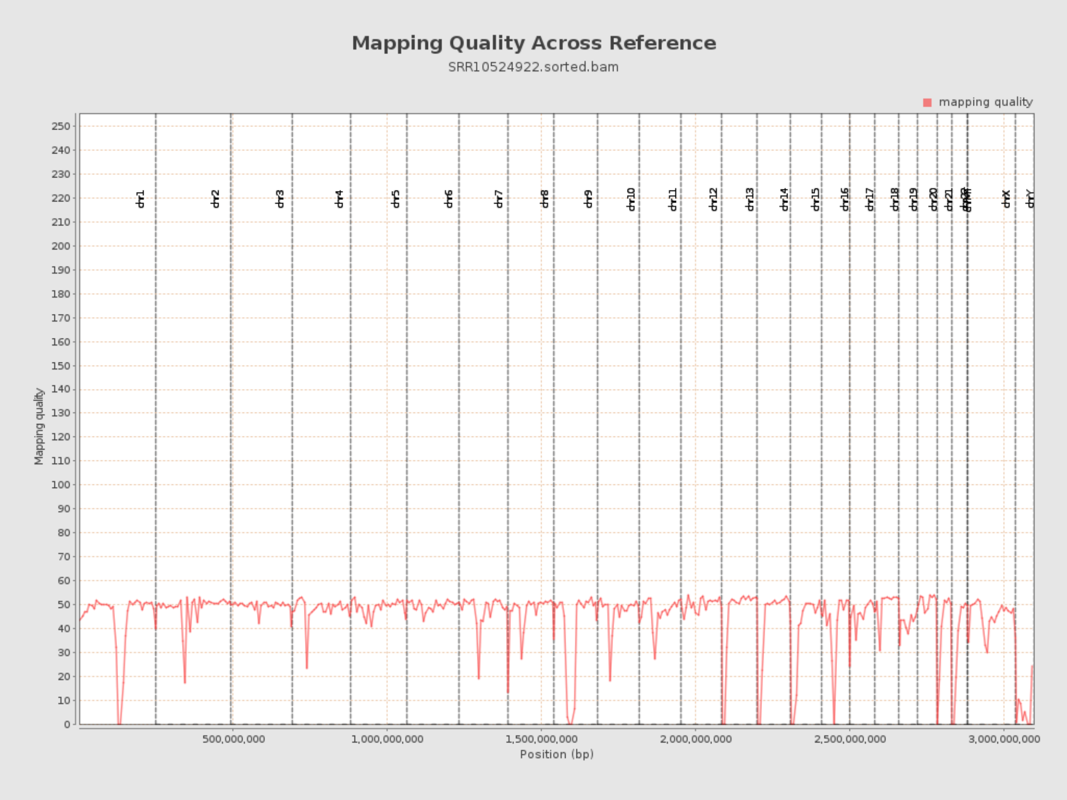
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram